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Diagnosis and prevention of cancer cell invasion

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Diagnosis and prevention of cancer cell invasion

Description

The present invention relates to diagnostic and therapeutic methods in the field of malignant disorders. More particularly, the invention provides methods of determining the invasivity of malignant disorders and methods for reducing the invasivity of malignant disorders including the prevention or treatment of cancer cell invasion.

In recent years it has been shown that overexpression of receptor tyrosine kinases (RTK) is in many cases associated with the development of malignant disorders, particularly cancer in mammals including human beings. For example, overexpression of the receptor tyrosine kinase AXL/UFO (ref. 1, 2; Genbank accession No. M 76125) has been implicated in the development of human hematological malignancies. Further, very recent data indicate that signalling of AXL and its ligand GAS6 is involved in angiogenesis, adhesion and survival of cancer cells (ref. 3, 4, 5, 6, 7, 8). There are, however, no data available which would suggest that overexpression of AXL is correlated with the invasivity and/or metastasis formation in malignant disorders.

The purpose of the present study was to establish expression profiles of genes particularly selected from protein kinases, phosphatases and other signalling genes in malignant disorders, particularly breast cancer in order to identify novel markers for invasivity and/or aggressiveness. A cDNA hybridization array was used to analyze gene expression profiles of seven highly invasive, fourteen weakly invasive breast cancer cell lines and three normal breast epithelial cell lines. Differences in gene expression between weakly and highly invasive breast cancer cell lines were identified, which enable the definition of a gene cluster correlating with the invasivity of a

breast cancer cell line. By using this cluster or combinations of genes therefrom, a discrimination of highly invasive breast cancer cell lines from weakly invasive breast cancer cell lines and normal breast epithelial cell lines is possible.

Thus, a first aspect of the present invention relates to a method of determining the invasivity of malignant disorders comprising determining the expression of at least one gene selected from the group consisting of AXL (Genbank M 76125), GAS 6 (Genbank L 13720), MMP14 (Genbank NM 004995), ADAM12 (Genbank AF 023476), ADAM17 (Genbank U 69611), MT3MMP (Genbank NM 005961), FGF2 (Genbank NM 002006), FGF5 (Genbank NM 004464), FYN (Genbank M 14333), LYN (Genbank M 16038), DDR2 (Genbank X 74764), TIMP1 (Genbank NM 003254), HB-EGF (Genbank NM 001945), SGK (Genbank Y 10032), RPS6RB1 (Genbank M 60724), MAP4K4 (Genbank XM 038748), SIRPα (Genbank Y 10375), and Annexin A2 (Genbank D 00017). It was found that a high expression of at least one of the above genes correlates with a high invasivity.

Preferably, the method comprises determining the expression of several of the above genes, e.g. determining the expression of at least two, three, four, five, six, seven or eight genes. More preferably, the method comprises determining the expression of at least the AXL/UFO gene (Genbank M 76125). Further, the method may comprise determining the expression of at least one further gene which is already known as a marker of invasiveness, such as CD44 (Genbank X 66733), vimentin (Genbank X 56134), CAV1 (Genbank Z 18951), CAV2 (Genbank AF 03572), MMP 1 (Genbank M 13509), MMP 2 (Genbank NM 004530), MMP9 (Genbank NM 004994), M-CSF (Genbank M 37435) and EPHA2 (Genbank M 59371).

A correlation between expression and invasivity of the above gene cluster and particularly the AXL gene was found in several types of malignant disorders, e.g. breast cancer, particularly primary breast cancer, prostate

cancer, kidney cancer and glioblastomas or other cancers of epithelial origin.

Further, it was found that stable overexpression of a dominant negative mutant of the AXL gene is capable of strongly suppressing cell invasiveness and migration indicating that inhibition of AXL function may block and loss of metastasis formation in highly invasive malignant disorders, such as breast cancer. Furthermore, a polyclonal antibody directed against the extracellular portion of AXL has a very strong inhibitory activity on the migration and invasivity of cancer cells, e.g. breast or prostate cancer cell lines. Moreover, overexpression of wildtype AXL in weakly invasive breast cancer and prostate cancer cell lines significantly increased their invasivity.

These data show that the AXL gene and protein is a promising new target for the prevention or treatment of malignant disorders, particulary for inhibiting the tumor invasivity and/or metastasis formation in malignant disorders.

Thus, a further aspect of the present invention relates to a method of reducing the invasivity of malignant disorders comprising inhibiting the AXL gene or protein. The method may comprise (i) inhibiting the receptor tyrosine kinase activity of the AXL protein, (ii) inhibiting the expression of the AXL gene, (iii) inhibiting the interaction between the AXL protein and its ligands, particulary GAS6 and/or (iv) inhibiting the interaction of AXL with downstream signal transducing factors.

The present invention relates to the diagnosis or the prevention and/or treatment of malignant disorders, particulary the tumor invasivity and/or metastasis formation in malignant disorders. Preferred examples of malignant disorders are cancers of the breast, prostate, kidney, colon, lung

and glioblastomas. More preferably, the malignant disorder is breast cancer.

In the diagnostic embodiment of the present invention the expression of invasivity-associated genes is determined qualitatively and/or quantitatively. The expression is determined in a sample comprising malignant cells, e.g. from a human tumour patient. The sample may be derived from tissue sections, biopsy samples etc. or from body fluids. Gene expression in the sample to be tested may be compared with gene expression in control samples, e.g. negative control samples from "normal" cells or weakly invasive malignant cells, and/or from positive controls, e.g. from highly invasive malignant cells.

Gene expression may be determined according to methods known in the art, e.g. on the mRNA or transcript level and/or on the protein level. Measurement of gene expression on the mRNA level may comprise reverse transcription and/or amplification reactions such as PCR. Preferably, gene expression is measured on a nucleic acid array, wherein nucleic acids from the sample to be tested, e.g. RNA or cDNA, is hybridized to an array of immobilized probes specific for the nucleic acids to be tested. A preferred example of a suitable nucleic acid array is described in PCT/EP 02/01073. Alternatively, gene expression may be determined by other methods, e.g. Northern blot hybridization.

Gene expression on the protein level may be determined by immunological methods using antibodies directed against the proteins encoded by invasivity-associated genes. The antibodies may be labeled directly or indirectly by known labeling groups such as radioactive, fluorescence, chemiluminescence or enzymatic groups such as known in the art.

The therapeutic embodiment of the present invention particulary relates to a method comprising the administration of an inhibitor of the AXL gene or

protein in an amount which is effective of reducing the invasivity of malignant disorders to a subject in need thereof. The subject is preferably a mammal, more preferably a human being.

The inhibitor of the AXL gene or protein may be an antibody, a biologically active nucleic acid or a low molecular weight compound, e.g. a peptide or a non-peptidic organic compound.

In a preferred embodiment the inhibitor is an antibody directed against the AXL protein. The term "antibody" relates to polyclonal antibodies and monoclonal antibodies, particularly to chimeric or humanized monoclonal antibodies or to human antibodies. Further, the term comprises antibody fragments, e.g. proteolytic fragments such as Fab, Fab' or $F(ab)_2$ fragments or recombinant fragments such as single chain antibody fragments, e.g. scFv fragments. Methods of manufacturing antibodies or antibody fragments as described above are known in the art.

In a further preferred embodiment the inhibitor is a biologically active nucleic acid, e.g. a DNA, an RNA or a synthetic nucleic acid analog. Preferred examples of biologically active nucleic acids are antisense nucleic acids, ribozymes or RNA interference molecules directed against the AXL gene or a transcript thereof. A further preferred example of a biologically active nucleic acid is a dominant-negative mutant of the AXL gene. Biologically active nucleic acids may be delivered by known procedures, e.g. by using viral or non-viral gene transfer vectors.

In a still further preferred embodiment the inhibitor is a peptidic compound, e.g. a peptide having a length of from 4 to 25 amino acids, a cyclic peptide, a peptide derivative or a peptide mimetic derived from such a peptide. Alternatively the low-molecular weight inhibitor may be a non-peptidic organic compound, e.g. an inhibitor of AXL kinase activity. Low-

molecular weight inhibitors may be obtained by screening suitable compound libraries in a method as described in more detail below.

Still a further aspect of the present invention relates to a pharmaceutical composition comprising as an active agent an inhibitor of the AXL gene or protein together with pharmacologically active diluents, carriers and/or adjuvants. This composition is particularly suitable for reducing the invasivity of malignant disorders and/or reducing the metastasis formation in malignant disorders. Depending on the type of inhibitor used as an active agent, the pharmaceutical composition may be a liquid, a solid, e.g. a powder, tablet etc., an emulsion or a suspension. The composition may be administered by injection, orally, topically, rectally, intranasally or by any other suitable means. The effective amount of the active agent in the composition may be determined by the skilled person without any undue burden depending on the type of compound and the disease to be treated.

The composition may comprise at least one further active agent. This at least one further active agent may be formulated together with the AXL inhibitor in a single composition or in a separate composition which is coadministered with the AXL inhibitor composition. The further active agent may be a cytotoxic or cytostatic agent such as doxorubicin, cis-platin, carboplatin, an anti-tumor antibody or any combination thereof.

Still a further aspect of the invention relates to a method of identifying and/or characterizing an inhibitor of the invasivity of malignant disorders comprising determining, if at least a test compound is capable of inhibiting the AXL gene or protein. More particularly, the method comprises determining, if a test compound is capable of binding to the AXL protein and/or reducing the AXL gene expression. The test compound may be derived from compound libraries, e.g. peptide or non-peptidic libraries which are subjected to a screening for AXL inhibitory activity. The screening method may comprise the use of a cell-based assay system, e.g.

a system using a cell capable of overexpressing the AXL gene. Additionally or alternatively, the method may comprise the use of a cell-free assay system, wherein the test compound is contacted with substantially purified AXL protein or a fragment thereof in order to determine binding of the test compound to the protein or fragment thereof.

Further, the invention shall be explained in more detail by the following figures and examples.

Figure 1. Morphology of normal and breast carcinoma (BC) cell lines when cultured on matrigel-matrix (3D outgrowth).

Cells were cultured on top of a Matrigel layer for 7–14 days. A, photographs representing the three basic morphologies are shown for the indicated BC cell lines. Magnification was x100 for MDA-MB-231, MDA-MB-435S, BT549 and MCF10A. Determination of the morphology of cells grown on Matrigel was carried out as described previously (10, 11, 12). Briefly, cells (5000 cells/well of a 96-well plate) resuspended in 50 µl of culture medium were plated on top of a preset Matrigel coating consisting of 70 µl of Matrigel (Becton Dickinson) diluted to 6 mg/ml in -RPMA basal medium salts. After polymerization on the top those 50 µl of Matrigel (1.0 mg/ml) was added. Colony outgrowth was monitored over the course of the experiment and photographed at 7–14 days using a Zeiss Axiovert 35 microscope equipped with OpenLab (UK) digital camera. The name of the respective cell line is indicated.

Figure 2. Classification of breast cancer cell lines by gene expression profile of known kinases and phosphatases. Common gene expression changes (Cluster AXL) in weakly invasive versus highly invasive BC cell lines.

Gene expression was measured by cDNA array hybridization of RNA (duplicate preparations) from each of the indicated cell lines, as described in "Materials and Methods." The 22 selected genes were differentially expressed in at least 75% of the weakly invasive BC cell lines, the highly invasive BC cell lines (red and green bar, subsequently), or both with median fold-changes of greater than 2-fold. The level of gene expression relative to MCF10A is shown by the colour and shade designated in the key at the bottom of the cluster. Each colour shade encompasses all of the values in the range spanned by the numbers beneath the scale. GenBank accession numbers (see Table 3) and descriptions for each gene, as well as the spot location on self-made arrays membranes are also provided (see separate Table 2 and 3 of genes). Confirmation studies were performed by Northern (AXL and GAS6) or RT-PCR analysis (Roche system for HER2 expression and amplification, not shown) using the same RNA preparations as in the array. Unless otherwise noted, agreement between the arrays and other methods was within 2-fold, correlative for the majority of samples; qualitative agreement with array underestimating fold-change by other methodology by at least 10-fold. The position of invasive and weakly invasive cell lines were indicated by colour bars, subsequently.

Figure 3A, B. Classification of primary breast cancer and their cell lines by gene expression profile of the known kinases and phosphatases.

Gene expression was measured by cDNA array hybridization of RNA (duplicate preparations) from each of the indicated cell lines and primary tumors, as described in "Materials and Methods." The 26 selected genes were differentially expressed in at least 75% of the weakly invasive BC cell lines, the highly invasive BC cell lines (red and green bar, subsequently), or both with median fold-changes of greater than 2-fold. The level of gene expression relative to normal breast tissues (mix of two) is shown by the colour and shade designated in the key at the bottom of the cluster. Each

colour shade encompasses all of the values in the range spanned by the numbers beneath the scale. GenBank accession numbers (see Table 3) and descriptions for each gene, as well as the spot location on self-made arrays membranes are also provided. Confirmation studies were performed by Northern (AXL and GAS6, not shown for primary tumors) or RT-PCR analysis (Roche system only for HER2 expression and amplification, not shown) using the same RNA preparations used in the array. Unless otherwise noted, agreement between the arrays and other methods was within 2-fold, correlative for the majority of samples; qualitative agreement with array underestimating fold-change by other methodology by at least 10-fold.

A. Not supervised array analysis of the normal breast tissues, primary tumors, normal breast and cancer cell lines. AXL cluster is included 18 genes (the correlation of expression is 0,51 or significant) the most of these genes were identified in breast cancer cell lines (see Fig. 2).

B. Classification primary tumors and breast cancer cell lines using only consensus invasiveness genes. All primary tumors and BC cell lines were applied for cluster analysis using 26 genes (belongs to the AXL cluster). Primary tumors and BC cell lines were recognised and most highly invasive (HI) BC cell lines belong to the same tree (with the exception of MDA-MB-231 and one primary tumor BC151, indicated by red bar).

Figure 4. Northern blot analyses of selected differentially expressed AXL/GAS genes.

mRNA (15 μg/lane) isolated from each of the indicated cell lines was analyzed for expression of the designated genes by hybridization with probes corresponding to the fragments deposited on the cDNA arrays. Expression levels for each mRNA relative to Ac745 (normal breast epithelial cells) are recorded beneath each band. The sizes (at right) corresponding to the major specific bands agree with those reported in the literature for each

mRNA. The same filters were used probed and re-probed for these analyses. Panel: A - expression AXL, B - GAS and C -β-actin mRNA. The levels of β-actin are shown for a representative filter as a control for equivalent sample load. mRNA was prepared from two independently grown cell cultures and tested for expression levels of the indicated genes.

Figure 5A and B. Morphology of BC cell lines MDA-MB-435S, BT549 and MDA-MB-231 (mock) or stably expressing dnAXL when cultured on Matrigel.

Cells were cultured on top of a Matrigel layer for 7–14 days.
A, photographs representing the three basic morphologies are shown for the indicated BC cell lines. B, Wound assays are shown for the MDA-MB-435S mock and dnAXL mutant clone 2. The position and treatment are indicated on the Fig. Magnification was x100.

Figure 6A, B and C. 3D outgrowth, migratory and invasive behaviour of BC cell line MDA-MB-435S, mock, stably expressing dnAXL or after treatment with anti-Ex-AXL antibody.

A. Cells were cultured on top of a Matrigel layer for 7–14 days (see legend to the Fig. 1). They were not treated or treated by antibody as indicated.
B. Invasive activities of the indicated BC cell line were measured in Boyden chambers by counting the number of cells that traversed the Matrigel (3-4 mg/ml)-coated filter in 20-36 h according to the procedure described in "Materials and Methods." Data are average values from at least two individual experiments containing triplicate points. Error bars.
C. Migration ability was assayed in parallel transwell chambers using filters without Matrigel under the same conditions as the invasion assay. Results shown are the averages of at least two experiments containing triplicate

points (error bars). Cell migration was evaluated also in a Boyden chamber in the absence of the Matrigel barrier. As expected, cell lines MDA231, MDA435S, and BT549 were considerably more motile than the weakly invasive cell line MCF7 (not shown).

Figure 7. Effect of AXL wt transfection on MCF7 breast cancer cells

A. The morphological effects of AXL wt infection and forced over-expression. The over-expression of AXL wt in MCF7 cells results in a change from compact cobblestone-shaped cells to irregularly shaped cells with many protruding extensions.
B. The effects of AXL wt infection on cell invasion were assayed in a Boyden chamber assay as described above (see Material and Methods). The clones MCF7-AXL wt were up to 30-fold more invasive than the empty vector-infected cells.
A total of 20,000 cells were seeded on a Boyden chamber for 36-48 h (with filters pores 8 μm, covered by matrigel matrix at concentration 3-4 mg/ml). Cells infected with AXL wt invade much sooner than cells infected with an empty vector control or dnAXL mutant form.

Example

1. Materials and methods

1.1. Tumor samples and cell lines

To avoid any bias of selection as to the type and size of breast cancer (BC) and others tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 72 patients undergoing surgery. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis

and an adjacent piece was quickly frozen in liquid nitrogen for mRNA extractions. The median age of patients at the time diagnosis was 55 years (range 29-81) and most of them were postmenopausal. Tumors were classified according to the WHO histological typing of breast tumors: ductal carcinomas, lobular carcinomas, mixed ductal-lobular carcinomas and medullary carcinomas. Pooled "normal" cDNA derived from normal breast mRNAs (3) was used as control and for normalisation. Expression profiles of protein kinases (PK) and phosphatases (PP) in "normal" cDNAs mentioned above were evaluated separately. In this study we also included 21 BC and 3 normal breast epithelial cell lines. The sources of the breast cancer cell lines were as follows: BT-20, BT-474, BT-483, BT-459, Du-4475, MDA-MB-134, -157, -175, -361, -436, -453, -468, SK-BR-3, and ZR-75-1, T-47D, MDA-MB-231, ZR-75-30 were obtained from the American Type Culture Collection (ATCC, Rockville, MD). MCF-7, clone and BC cell line DAL were supplied by SUGEN (Redwood City, CA). The HBL-100 cell line was from ATCC. This cell line was derived from normal tissue but contains tandemly integrated SV-40 sequences (9). Cultures were maintained in exponential growth in RPMI 1640 medium, supplemented with 6 mM glutamine, 10 μg/ml human insulin and 10% Fetal calf serum (FCS) (CSL, Parkville, Australia). Normal breast epithelial cell strains MCF10A, MCF10 T-24 and MCF10 neo were provided by Dr. B. Gilles (Arizona Cancer center). Ac745 was provided by Dr. M. Stampfer and grown in the DMEM F12 medium supplemented by the condition medium of Hs578Bst, Insulin, Hydrocortisone, EGF, Cholera toxin, vitamins and antibiotics.

Cells were free from Mycoplasma contamination.

1.2. Isolation and fractionation of RNA and DNA.

Total RNA and genomic DNA was isolated from the same cell pellet by lysis in guanidinium isothiocyanate solution (GTS buffer: 4 M guanidinium isothiocyanate, 25 mM sodium citrate pH 7.0, 0.5% Sarkosyl, and 0.1 M ß-mercaptoethanol) followed by phenol-chloroform extractions. Total RNA was isolated using standard methods (Sambrook et al., [1989]) with modifications. DNA was collected and extracted twice with an equal volume of phenol:chloroform:isoamylalcohol (25:24:1). RNA and DNA were isolated from each cell line on a minimum of 3 independent occasions.

Total and mRNA integrity and cDNA complexity was controled by agarose gel electrophoresis and Norhthern blots using specific probes. Some mRNA extraction was performed using the OligoTex mRNA isolation Kit (Quagen, Biotech, Germany). Cell pellets were resuspended in lysis/binding buffer, vortex-mixed briefly, passed three times through a 21G needle and applied to a spin lysate column and centrifuged at 13,000g for 3 min. The lysate was then mixed gently with Oligo-dT cellulose (Stratagene Inc.) and applied to a pre-wetted Oligotex molecular biology column (Quagen Biotech). The column was washed three times with lysis/binding buffer and four times with wash buffer before eluting the mRNA with pre-warmed (65C) elution buffer. The quantity of mRNA was measured using the OD260.

1.3. cDNA arrays preparations

PK and PP gene expression was analyzed by hybridization on nylon filters arrays with radioactive targets (cDNA). The arrays contained 645 genes encoding kinases, phosphatases and others signalling proteins: ligands, adaptors, transcription factors, metalloproteinases/ADAMs, apoptosis related genes and 11 house keeping genes (the list is available at http://www.biochem.mpg.de or ullrich@biochem.mpg.de). Their identity

was verified by sequencing of plasmid DNA and compared with GenBank sequence information. Identity of PK and PP was conformed for all clones spotted on nylon filters ones, or in duplicate. For normalisation purpose, the GFP gene was spotted two times as well as genomic and vector DNA. Purification of plasmids was done using a plasmid purification kit (Qiagen, Germany).

1.4. cDNA array hybridization

Filters were initially pre-washed in 0.5% SDS for 5 min, with agitation. In 10 ml of the pre-hybridisation solution was included Yeast tRNA. Human Cot-1 DNA (BRL/Life technologies) was used in the hybridization step which was performed in a Roller bottle (Hybaid Inc.) for 16 h in a roller oven at 65°C. Labelled probe was denatured for 10 min at 100°C and then placed immediately into the hybridisation mixture which was incubated for a further 18 h at 65°C. After 18 h, the hybridisation mixture was discarded and the array was washed twice in 2 sodium chloride: sodium citrate (SSC) buffer, 0.2% SDS for 20 min at 42°C with continued rotation in the incubator. A third wash was performed in 0.2xSSC, 0.1% SDS for 15-60 min at 65°C in a plastic box with horizontal shaking. After the third wash, the filter was placed on a piece of moistened Whatman paper and covered with Saran wrap. The array was then placed into an imager cassette with a Phosphorimager storage screen (Fuji, Japan) and exposed for 2 days.

1.5. Image acquisition and analysis.

Exposed phospho-imager storage screens were scanned once on a Phosphoimager Scanner (Fuji) at a resolution of 50 microns and were visualised using MacBAS 2000 (Fuji). Images were imported into ArrayVision V(Canada) for analysis by a software protocol. Mapping of individual elements to an internal reference database was achieved by

aligning the images onto a software-based matrix using a total of 4 control elements representing total genomic control DNA, GFP, and vector. Normalisation was performed by multiplying the raw intensity for each data element by a normalisation factor equal to the average raw intensity for all the vector elements divided by 100 (this value is the average raw intensity for all elements, derived from a large number of different hybridizations performed by us the development of the arrays). Software-based pair-wise comparisons of the normalised images were made against the image obtained from hybridisation of labelled cDNA taken from pooled "normal" cDNA derived from normal breast RNAs, immortal (preneoplastic) breast epithelial cell lines, as indicated above. Changes in expression levels were calculated using normalised intensities and given as ratios (positive ratios indicated an increase in transcript levels, negative ratios indicated a decrease in transcript levels) and were visualised by Scatter-blot graphics and TreeView program (13-16).

1.6. Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridizations with the same cDNA on two independent arrays, or two independent hybridizations with cDNA prepared from the same RNA. In each case, the results showed good reproducibility with respective correlation coefficients 0.96, 0.98 and 0.98 (data not shown). The reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential. Subsequent analysis was done using Excel and statistical software. The search for genes with expression levels correlated with tumor parameters was done in several successive steps. First, genes were detected by comparing their median expression level in the two subgroups of tumors differing according to parameters of interest. We used the median values rather than the mean values because of the high variability of the expression levels for many genes, resulting in a standard deviation expression level similar or superior

to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics and, finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of HER2 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels with the number of axillary nodes involved.

1.7. Cluster analysis

The data from this study were analyzed and displayed as described (13-16). Briefly, a hierarchical clustering algorithm produces a table of results wherein the elements/cDNAs of the array (representing specific genes) are grouped together based on similarities in their patterns of gene expression. The same algorithm is applied to cluster the experimental samples (i.e., cell lines and tumors) according to the similarities in their overall patterns of gene expression. The data tables, thus ordered, are presented graphically as colored images. Along the vertical axis, the genes analyzed are arranged as ordered by the clustering algorithm, so that the genes with the most similar patterns of expression are placed adjacent to each other. Along the horizontal axis, experimental samples are similarly arranged such that those with the most similar patterns of expression across all genes are placed adjacent to each other. The colour of each cell/square in this tabular image represents the measured expression ratio of each gene in question. The colour saturation is also directly proportional to the magnitude of the measured gene expression ratio with the brightest red squares having the highest T/N ratio (i.e., >8-fold difference), the brightest green squares having the lowest T/N ratio, black squares indicating a ratio of approximately 1, and grey squares indicating insufficient data quality.

1.8. RNA analysis by Northern-blot

We used standard protocol of Northern-blot analysis for detection of the expression AXL and GAS6 genes in preparation of some breast cancers and all breast cancer cell lines. The loading RNA samples were verified by re-hybridization of filters with a human β-actin probe.

1.9. Chemoinvasion and Migration Assays

The chemoinvasion assay was carried out using a modification of the method of Albini et al. (10). After trypsinization, cells (20.000) were plated on Matrigel-coated (150 μl of 4.0 mg/ml) 8-μm polypropylene filter inserts in Boyden chambers (Biocoat Matrigel Invasion Chamber, Becton Dickinson, Bedford, MA or Nunc 10mm tissue culture inserts, Naperville, IL). The bottom chamber contained 0.55 ml of NIH3T3-conditioned media, produced as described by Albini et al. or normal growth media for some cell lines.

BC cell lines obtained from the ATCC were trypsinized, centrifuged, and resuspended at 4 x 10^5cells/ml in RPMI medium containing 10% FBS. The remaining cell lines were resuspended in their regular growth medium.

After 20-36 h, the cells remaining in the insert were removed with a cotton swab, and the cells on the bottom of the filter were counted using different protocols: fixed in Diff-quick (American Scientific Products, McGraw Park, IL) and treated with RNase A (at 50 μg/ml for 20 min at 37°C) before staining with propidium iodide (10 μg/ml in PBS) for 1 min at room temperature (RT). The dried filters were removed and mounted on slides with Cytoseal 60 mounting media (Stephens Scientific, Kalamazoo, MI). Individual propidium iodide-stained nuclei on the filters were counted. Most results were obtained using trypsinization and counting of the cells.

Triplicate samples were counted in each experiment. Outlying values were eliminated from calculations of average invasive activity.

For invasion assays in presence of antibody, cells were seeded on Matrigel and, when attached, the indicated antibody was added to the medium. The antibody was present in the upper chamber for the entire duration of the assay; at the end of the assay, cell viability in the upper chamber was assessed by Trypan blue. Migration activity was determined following the procedure described for the invasion assay except that the cells were plated on top of uncoated 8-μm pore polypropylene filters in the Boyden chambers.

1.10. Matrigel Outgrowth

Determination of the morphology of cells grown on Matrigel was carried out as described previously (10). Briefly, cells (5000 cells/well of a 96-well plate) resuspended in 50 μl of culture medium were plated on top of a pre-set Matrigel coating consisting of 70 μl of Matrigel (Becton Dickinson) diluted to 6.0 mg/ml in -RPMI basal medium salts. After polymerization on the top of these diluted 50 μl of Matrigel (1.0 mg/ml) were added. Colony outgrowth was monitored over the course of the experiment and photographed at 7–14 days using a Zeiss AxioVert 35 microscope equipped with a OpenLab (UK) digital camera.

1.11. Wound assay

After overnight starvation, wounds were made on confluent cell monolayers with a plastic tip. MDA-MB-345S-mock and MDA-MB-435-dnAXL, clone 2 cells were treated with culture medium (10% FCS) and culture medium containing GAS6 (200 ng/ml) for 12, 24 and 48 h, before taking pictures (phase contrast). To quantify cell migration, three randomly chosen regions of a wound (1 mm long) were photographed at a

magnification of 40X; a mean wound width was measured every 20 μm, and an average percent wound closure was calculated. Three independent wounds were examined per sample and a mean percent wound closure was calculated.

1.12. The treatment of cells with antibody

Breast cancer cells (5000 for the 3D outgrowth assay and 20000 for the invasion assay in a Boyden chamber) were treated by Ex-AXL polyclonal antibody (200 μg/ml) using 50 μl of antibody and 500 μl cell suspension. Cells were incubated with antibody 60 min at RT and then washed in PBS at RT. Plating of cells and the following 24 h treatment interval were performed with the same concentration of Ex-AXL antibody.

1.13. Infection of BC cells with recombinant retroviruses

AXLwt and dn-AXL mutant forms of the viruses were obtained according to a standard protocol (31) with modifications. Briefly, pLXSN-AXLwt and pLXSN-dnAXL were cloned via EcoRI/BamHI and NotI/XbaI sites, subsequently.

The packaging cell line Phoenix A was transfected with these vectors using calcium phosphate. The supernatant of transfected Phoenix A cells was collected and filtered trough a 0.45-μm filter. for the infection of the human cancer cell line, cells were incubated with viral supernatant for 24 h. After 48 h, medium was replaced with medium containing 400 μg/ml G148. For further selection, cells were incubated with G418 for 14 days. Polyclonal and monoclonal cell lines were generated by limited dilution. AXL expression was monitored by Western blot and array analysis. Polyclonal and three monoclonal cell lines with similar expression levels of AXL wt and dn-AXL were chosen for further experiments.

1.14. Antibodies

AXL/UFO-specific antibodies were generated by immunization of rabbits with recombinant GST-AXL extra-cellular domain fusion protein containing amino acid residues 1-410 (AXL-Ex). The recombinant GST-AXL-Ex protein was stably secreted by transfected HEK293 cells (vector pcDNA3-GST). Culture medium was collected and GST-AXL-Ex protein purified using standard GST-tag protocol (Pharmacia, Sweden). AXL-Ex polyclonal antibodies were partially purified on GST-Sepharose affinity columns.

2. Results

The purpose of this study was to establish expression profiles of protein kinase, phosphatase and signalling genes in breast cancer cells with the objective of identifying novel markers for breast cancer aggressiveness. cDNA hybridization arrays were used to analyze the gene expression profiles of 14 weakly, 7 highly invasive breast cancer cell lines and 3 normal breast epithelial cell lines (Table 1, Fig. 1, 3D growth of invasive BC cell lines and control).

Table 1 Characteristics of the breast cancer cell lines used to generate the consensus of invasiveness

Cell line	Specimen origin *a*	Tumorigenicity *b*	Matrigel morphology *c*	Marker gene expression *d*		
				ER-	E-cad	Vim
Weakly invasive						
ZR-75-1						
T47D	Infiltrating ductal Ca; PE	+*e*	Fused	+	+	-
ZR75-1	Infiltrating ductal Ca; ascites	+*e*	Fused	+	+	-
MCF7	Breast adenocarcinoma; PE	+*e*	Fused	+	+	-
MDA361	Breast adenocarcinoma; brain met	+*e*	Fused	+	+	-
BT474	Invasive ductal Ca; PT	+*e*	Fused	+	+	-
BT20	Breast adenocarcinoma: PT	+	Fused	ND	-	
MDA468	Metastatic adenocarcinoma; PE	+	Fused	-	-	
SKBR3	Breast adenocarcinoma; PE	+	Spherical	-	-	-
MDA453	Metastatic breast Ca; PE	-	Spherical	-	-	-
BT483						
MDA175						
Du44-75						
DAL						
ZR-75-30						
HBL-100						
Highly invasive						
MDA435S	Metastatic ductal adenocarcinoma	+, met	Stellate	-	-	+
BT549	Papillary invasive ductal Ca; PT	-	Stellate	-	-	+
Hs578T	Ductal Ca; PT	+, met	Stellate	-	-	+

MDA231	Breast adenocarcinoma: PE	+, met	Stellate
MDA436	in progress	- - +	Stellate
MDA415	in progress		
MDA157	in progress		Stellate

Remarks:

a) Specimen origin and pathological assessment information were obtained from the ATCC catalogue. PT, primary tumor; PE, pleural effusion; Ca, carcinoma.

b) Tumorigenicity data was reported in the ATCC catalogue or in Ref. 17. +, palpable tumors produced as xenografts in athymic nude or SCID mice; -, nontumorigenic; met, metastatic cell lines as reported by Refs. 18 and 19.

c) Description of the morphology of cells cultured in Matrigel and their activity in the Boyden chamber invasion assay was taken from Ref. 10.

cDNA microarray membranes, containing 650 genes were used in these studies. Differences in gene expression between weakly and highly invasive BC cells were identified that enabled the definition of "consensus of invasiveness" for each invasive phenotype (Fig. 2, Cluster AXL, correlation >0.71). Highly invasive BC cell lines (BT549, MDA-MB-231, MDA-MB-436, MDA-MB-415, Hs578T, MDA-MB-157 and MDA-MB-435S) over-expressed AXL and show a defined gene expression profile that discriminate them from weakly invasive BC cell lines and "normal" breast epithelial cells. These cluster included genes already known as markers of invasiveness (CD44, VIM, CAV1, 2 and MMPs (Ref. 20-27)). Some of these genes have only been considered for association with cancer cell invasiveness (M-CSF and EPHA2 (Ref. 28-30) and Table 2). Other genes of the cluster were identified for the first time as genes associated with cancer cells aggressiveness: AXL, GAS, MMP14, Adam12, Adam17, MT3MMP, FGF2 and 5, Fyn, Lyn, DDR2, TIMP1, HB-EGF, SGK, S6KII, MAP4K4, SIRPα and Annexin 2.

Remarkably, no one of these BC cell lines did express estrogen receptor (see Fig. 3, as indicated for the BC cell lines characteristics). Cluster AXL of the co-expressed genes was identified in primary BC (Fig.3) and others tumors and cancer cell lines (kidney, prostate and glioblastomas) as well (data not shown). The expression of the AXL and GAS genes in invasive BC cell lines were conformed by Northern-blot hybridization (Fig. 4).

The dominant negative mutant of the AXL gene (dnAXL) which was stable over-expressed in highly invasive BC cell lines strongly suppressed invasiveness, migration and survival of the several BC cell lines: MDA-MB-435S, BT549 and partially MDA-MB-231 (Fig. 5A and B). All clones having stable dn-AXL expression had 3D-growth on the Matrigel matrix like non-invasive or weakly invasive breast cancer cell lines, for example, MCF7. The dn-AXL expression significantly inhibits GAS6 signalling and results in reduced or lacking AXL phosphorylation upon GAS treatment. ERK2 signalling in these cells was also blocked.

A polyclonal antibody directed against extracellular portion of AXL (containing amino acids residues 1-410, Ex-AXL) alters the cell morphology (Fig. 6A) and has very strong inhibitory activity on the migration and invasion of the MDA-MB-435S and BT549 BC cell lines (Fig. 6B and C). Similar results were obtained with the prostate cancer cell line PPC1. Moreover, over-expression of wild-type (wt) AXL in the weakly invasive BC cell line MCF7 and prostate cancer cell line LNCaP resulted in a transformation in to a highly invasive phenotype.

These data show that AXL/GAS play a key role in human cancers by influencing tumor cell invasion. AXL protein is a new target for cancer diagnosis and treatment (anti-invasiveness). For example, expression of dnAXL in cancer cells can prevent them from invasion and development of metastases. Further, genes of AXL-cluster (listed in Tab. 2) can be used as diagnostic tool for the detection of the pre-invasive stage development in primary tumours, particularly in primary tumours of breast, prostate, kidney and glioblastomas.

3. Discussion

The fact that RTK AXL as a single gene is sufficient to induce tumor metastasis in experimental systems is surprising, because it stands in contrast to the current view that the acquisition of a metastatic phenotype is a multistep process involving several genetic and epigenetic events.

Both benign and malignant tumours grow in an uncontrolled way. But only cells of malignant tumours invade surrounding tissues and travel to distant organs (metastasize). An understanding of the molecular basis for this aggressiveness could lead to therapies that block the transition of a tumour from benign to malignant, and keep local disease in check. We have now identified proteins called AXL and GAS as a receptor-ligand pair in a molecular checkpoint that regulates not only the invasiveness but also the surviving and movement of tumour cells - the trio of characteristics required for metastasis. The dn-AXL/GAS6 complex also suppresses tumor cells anti-apoptotic capability.

Our data show that GAS treatment of the BT-549 cells (stable expression of dn-AXL) in the presence of serum is not able to induce activation of ERK1/2 MAPK. Thus, this signalling pathway is effectively blocked AXL suppression.

4. Conclusions

1. Using cDNA array analysis of BC cell lines and primary tumors a "consensus of invasiveness" (cluster AXL) has been identified. This consensus of invasiveness, comprising 32 genes, can be used to predict the aggressiveness of cancer cells and primary tumors.

2. A dominant negative mutant of AXL (dn-AXL) strongly suppresses the invasion of highly invasive breast cancer cell lines and also increases their sensitivity to serum withdrawal (apoptosis). A polyclonal antibody directed against extracellular

portion of AXL (containing amino acids residues 1-410, Ex-AXL), is able to suppress the aggressiveness of the treated cancer cells.

3. RTK AXL as a single gene is sufficient to induce breast cancer cell invasiveness in experimental systems (see 2 and data on model systems BC - MCF7-wt AXL and prostate cancer cell line - LNCaP-wt AXL). This result is in contrast to the current view that the acquisition of a metastatic phenotype is a multistep process involving several genetic and epigenetic events.

4. RTK AXL is a good candidate for "Signal-transduction therapy" treatment strategies in which key pathways for hyperactive cellular signalling that cause cancer invasiveness and metastasis are targeted. The suppression of AXL signalling function by a dn-AXL mutant and/or by treatment with an inhibitory antibody cannot be bypassed by collateral or compensatory pathways.

5. Suppression of AXL gene expression in tumor therapy may be carried out by inhibition of AXL on the gene or transcript level, e.g. gene transfer of mutants, antisense molecules, ribozymes, siRNA, RNAi, or AXL gene expression supressors or on the protein level, e.g. by low molecular weight AXL kinase inhibitors, AXL analogues, e.g. Ex-AXL fusion proteins such as a fusion of Ex-AXL with an JgG1 Fc fragment (ref. 32) or inhibitory antibodies. Further, suppression of AXL gene expression may be effected by AXL signal inhibitors, e.g. downstream inhibitors.

Tab. 2 Consensus of invasiveness

Breast cancer cell lines and control

No	Genes of AXL cluster	Known function or involvement
1	AXL/GAS	proliferation, adhesion, antiapoptotic function, not yet associated with invasion
2	HBEGF	heparin-binding EGF
3	EPHA2	involved in breast cancer, prostate cancer, melanomas, glioblastomas vascularization
4	S6KII	STK, ribosomal S6 kinase 2, not yet associated with invasion
5	SGK	STK, glucocorticoid-regulated kinase, antiapoptotic function, involved in survival of cells
6	ADAM17	TACE involved in shedding of TNF alpha receptor
7	Lyn/Fyn	SRC-family kinases
8	MAP4K4	STK, activates JNK (but not p38 and ERKs), may be involved in TNFalpha signalling, similar to SLK
9	CD44/META1	marker of cancer cells invasiveness
10	ADAM12	interacts with integrins, coexists with SRC and GRB2 in membrane ruffles, cytopl.domain involved in signalling via SH3
11	Caveolin 1, 2	key role in signalling, associated with cell transformation, promote cell invasion
12	M-CSF	ligand for CSF-R1, vasculogenesis, constitutivelly expressed by invasive breast cancer cells
13	MMP14	unic expression in endothelial cells, specific for CD44 shedding
14	Vimentin	associated with cell transformation, promotes cell migration and invasion, marker of epithelial-mesenchymal transition of cancer cells
15	SIRP alpha	adhesion, signalling, migration, involvement in invasion is unknown

Tabl. 3.

O	Spot labels(HUGO classification)	Accession	GenBank/Link	Publication
1	AXL (AXL receptor tyrosine kinase)	M76125	M76125	Mol. Cell. Biol. 11 (10), 5016-5031 (1991)
2	ADAM12 (a disintegrin and metalloproteinase domain 12=meltrin alpha)	AF023476	AF023476	J. Biol. Chem. 273 (1), 157-166 (1998)
3	ADAM17 (a disintegrin and metalloproteinase domain 17=TACE)	U69611	U69611	Nature 385 (6618), 729-733 (1997)
4	ANXA2 (Annexin A2, p35 src-binding)	D00017	D00017	Cell 46 (2), 191-199 (1986)
5	CAV1 (caveolin 1, caveolae protein, 22kD)	Z18951	Z18951	FEBS Lett. 314 (1), 45-48 (1992)
6	CAV2 (caveolin 2)	AF035752	AF035752	Proc. Natl. Acad. Sci. U.S.A. 93 (1), 131-135 (1996)
7	CD44 (antigen= involved in matrix adhesion)	X66733	X66733	J. Invest. Dermatol. 99, 381-385 (1992)
8	DDR2 (discoidin domain receptor family, member 2)	X74764	X74764	Oncogene 8 (12), 3433-3440 (1993)
9	FGF2 (fibroblast growth factor 2 (basic))	NM002006	NM_002006	EMBO J. 5 (10), 2523-2528 (1986)
10	FGF5 (fibroblast growth factor 5)	NM004464	NM_004464	Mol. Cell. Biol. 8 (8), 3487-3495 (1988)
11	EPHA2 (EphA2=ephrin type-a receptor 2L)	M59371	M59371	Mol. Cell. Biol. 10 (12), 6316-6324 (1990)
12	GAS6 (AXL ligand, growth arrest-specific 6)	L13720	L13720	Mol. Cell. Biol. 13 (8), 4976-4985 (1993)
13	FRK (fyn-related kinase)	U00803	U00803	Gene 138, 247-251 (1994)
14	(HB-EGF)DTR (heparin-binding epidermal growth factor-like growth factor)	NM001945	NM_001945	Science 251, 936-939 (1991)
15	LYN (tyrosine-protein kinase)	M16038	M16038	Mol. Cell. Biol. 7 (1), 237-243 (1987)
16	PTPNS1 (PTP, non-receptor type substrate 1)	Y10375	Y10375	Nature 386 (6621), 181-186 (1997)
17	MMP1 (matrix metalloproteinase 1=interstitial collagenase)	M13509	M13509	J. Biol. Chem. 261, 6600-6605 (1986)
18	MMP14 (matrix metalloproteinase 14 (membrane-inserted))	NM004995	NM_004995	Nature 370 (6484), 61-65 (1994)
19	MMP2 (matrix metalloproteinase 2, gelatinase A)	NM004530	NM_004530	J. Biol. Chem. 263, 6579-6587 (1988)
20	MMP9 (matrix metalloproteinase 9=gelatinase B)	NM004994	NM_004994	J. Biol. Chem. 264 (29), 17213-17221 (1989)
21	MAP4K4(mitogen-activated protein kinase kinase kinase kinase 4)	XM038748	NT_022171	Direct Submission
22	MT3MMP, or MMP16 (matrix metalloproteinase 16 (membrane-inserted))	NM005941	XM_042409	J. Biol. Chem. 270 (39), 23013-23020 (1995)
23	TIMP1 (tissue inhibitor of metalloproteinase 1)	NM003254	NM_003254	Nature 315 (6022), 768-771 (1985)
24	VIM (vimentin)	X56134	X56134	Nucleic Acids Res. 18 (22), 6692 (1990)
26	SGK (serum/glucocorticoid regulated kinase)	Y10032	Y10032	Proc. Natl. Acad. Sci. U.S.A. 94(9) , 4440-4445 (1997)
26	RPS6KB1 (ribosomal protein S6 kinase, 70kD, polypeptide 1)	M60724	M60724	Mol. Cell. Biol. 11 , 5541-5550 (1991)
27	FYN (proto-oncogene tyrosine-protein kinase (syn)	M14333	M14333	Proc. Natl. Acad. Sci. U.S.A. 83, 5459-5463 (1986)

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Claims

1. A method of determining the invasivity of malignant disorders comprising measuring the expression of at least one gene selected from the group consisting of AXL, GAS, MMP14, ADAM12, ADAM17, MT3MMP, FGF2, FGF5, FYN, LYN, DDR2, TIMP1, HB-EGF, SGF, S6KII, MAP4K4, SIRPα and Annexin 2, wherein a high expression correlates with a high invasivity.

2. The method of claim 1 comprising measuring the expression of at least the AXL gene.

3. The method of claim 1 or 2, wherein the malignant disorder is cancer, particularly selected from breast cancer, prostate cancer, kidney cancer, lung cancer, colon cancer, glioblastomas and other cancers.

4. The method of any one of claims 1-3, wherein the expression is determined on the mRNA level.

5. The method of claim 4, wherein the expression is determined on a nucleic acid array.

6. The method of any one of claims 1-3, wherein the expression is determined on the protein level.

7. The method of claim 6, wherein the expression is determined by an immunoassay.

8. A method of reducing the invasivity of malignant disorders comprising inhibiting the AXL gene expression and/or protein function.

9. The method of claim 8 comprising inhibiting the receptor tyrosine kinase activity of the AXL protein.

10. The method of claim 8 comprising inhibiting the expression of the AXL gene.

11. The method of claim 8 comprising inhibiting the interaction between the AXL protein and its ligands.

12. The method of any one of claims 8-11 comprising the administration of an inhibitor of the AXL gene or protein in an amount which is effective of reducing the invasivity of malignant disorders to a subject in need thereof.

13. The method of claim 12, wherein the malignant disorder is cancer, particularly selected from breast cancer, prostate cancer, kidney cancer, lung cancer, colon cancer, glioblastomas and other cancers.

14. The method of claim 12 or 13, wherein the subject is a mammal, particularly a human.

15. The method of any one of claims 12-14, wherein the inhibitor is an antibody directed against the AXL protein.

16. The method of any one of claims 12-14, wherein the inhibitor is an antisense nucleic acid, a ribozyme or an RNA interference molecule directed against the AXL gene or a transcript thereof.

17. The method of any one of claims 12-14, wherein the inhibitor is a dominant-negative mutant of the AXL gene.

18. A pharmaceutical composition comprising as an active agent an inhibitor of the AXL gene or protein together with pharmacologically active diluents, carriers and/or adjuvants.

19. The composition of claim 18, wherein the inhibitor is an antibody directed against the AXL protein.

20. The composition of claim 18, wherein the inhibitor is an antisense nucleic acid, a ribozyme or an RNA interference molecule directed against the AXL gene or a transcript thereof.

21. The composition of claim 18, wherein the inhibitor is a dominant-negative mutant of the AXL gene.

22. The composition of any one of claims 18-21 for reducing the invasivity of malignant disorders.

23. The composition of any one of claims 18-22 for reducing the metastasis formation in malignant disorders.

24. The composition of any one of claims 18-22 comprising at least one further active agent.

25. The composition of claim 24, wherein the further active agent is a cytotoxic or cytostatic agent.

26. A method of identifying and/or characterizing an inhibitor of the invasivity of malignant disorders comprising determining, if a test compound is capable of inhibiting the AXL gene or protein.

27. The method of claim 26 comprising determining, if a test compound is capable of binding to the AXL protein and/or reducing the AXL gene expression.

28. The method of claim 26 or 27, wherein a cell-based assay system is used.

29. The method of claim 26 or 27, wherein a cell-free assay system is used.

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Abstract

The present invention relates to diagnostic and therapeutic methods in the field of malignant disorders. More particularly, the invention provides methods of determining the invasivity of malignant disorders and methods for reducing the invasivity of malignant disorders including the prevention or treatment of cancer cell invasion.

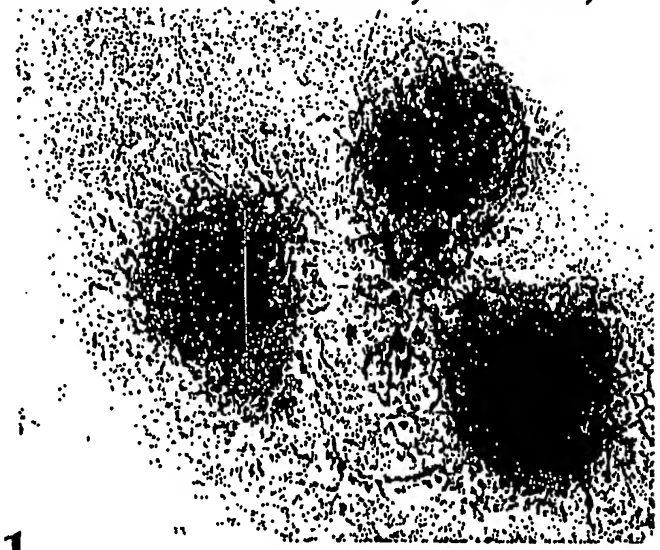
ld 17.07.2002

3D growth of invasiv BC cell lines on Matrigel(6mg/1mg/ml)

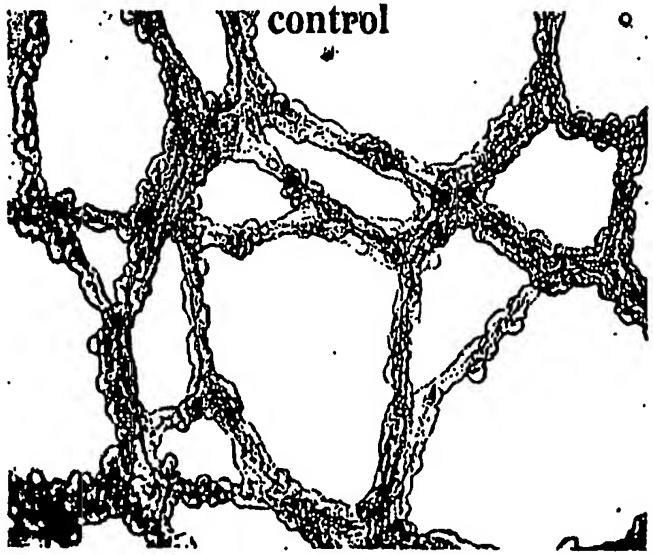
MDA-MB-231 (branched, invasive)

MBA-MB-435S (branched-stellate, invasive)

BT-549 (stellate, invasive)



MCF10A (duct-like pattern, non invasive), control



all x 100

Fig. 1

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17. Juli 2002
17. Juli 20

Fig. 2

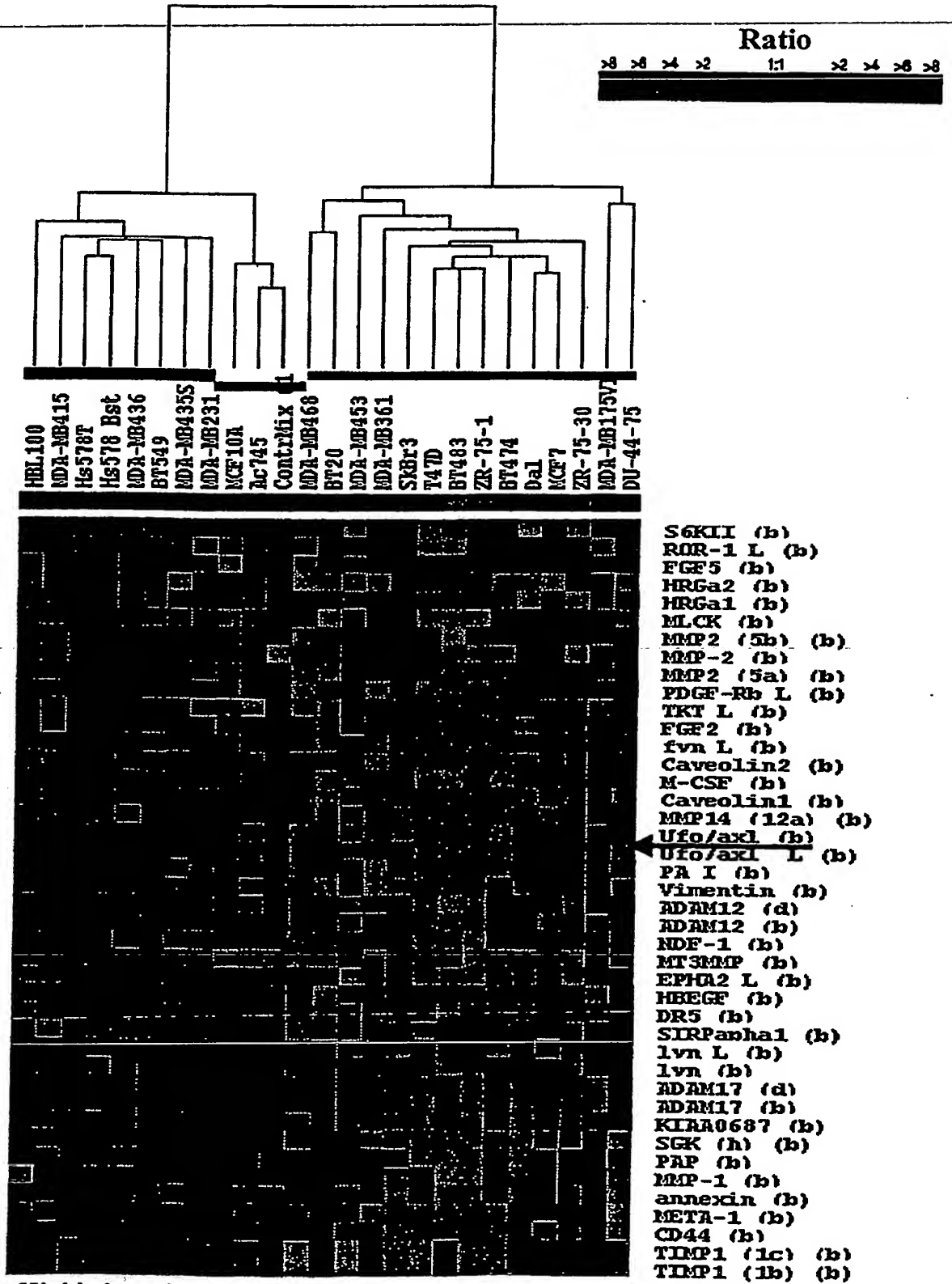
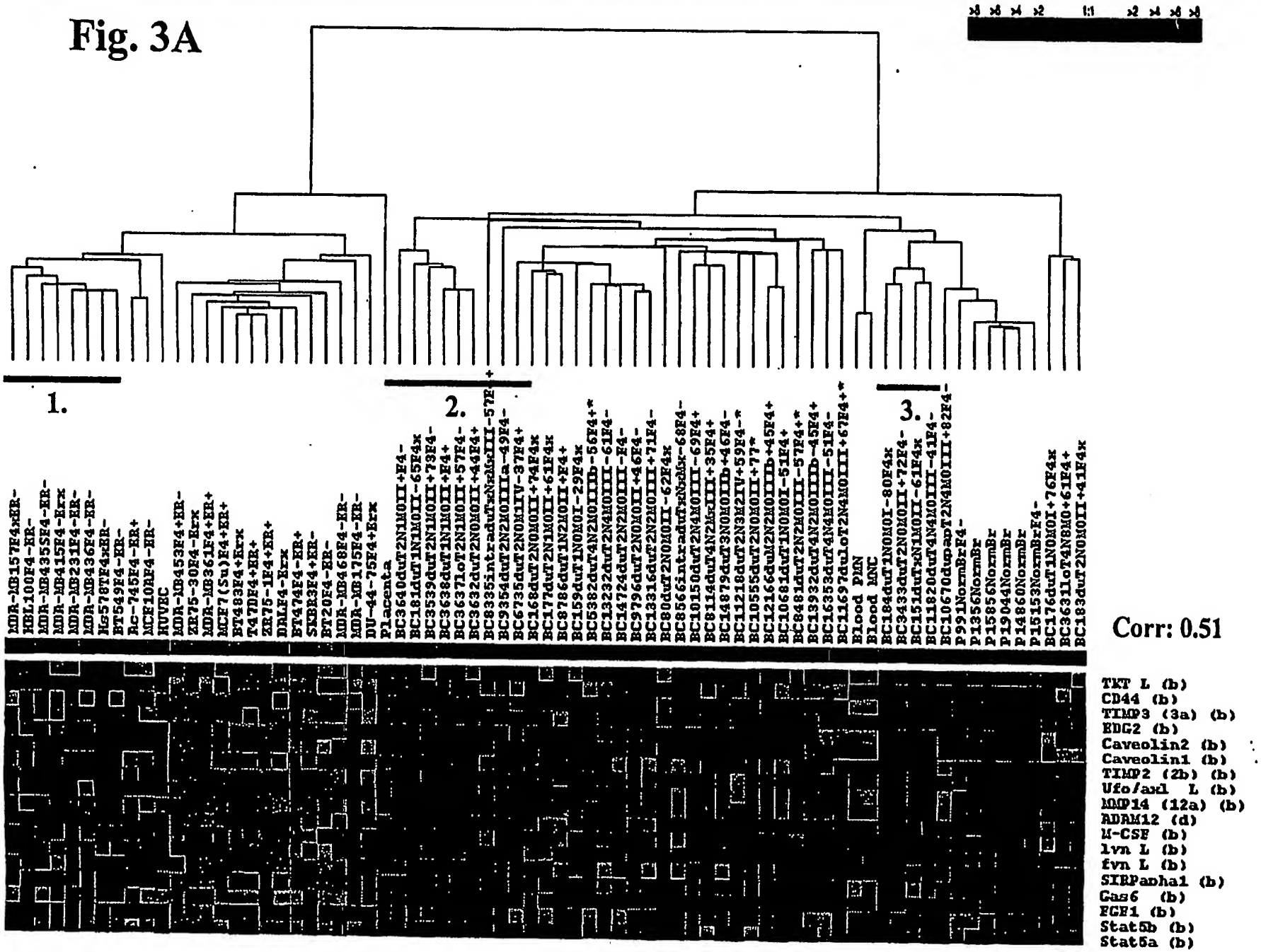

Ratio
>8 >6 >4 >2 1:1 >2 >4 >6 >8
HBL100
MDA-MB415
Hs578T
Hs578 Bst
MDA-MB436
BT549
MDA-MB435S
MDA-MB231
MCF10A
Ac745
ContrMix
MDA-MB468
BT20
MDA-MB453
MDA-MB361
SKBr3
T47D
BT483
ZR-75-1
BT474
Dal
MCF7
ZR-75-30
MDA-MB175V1
DU-44-75
S6KII (b)
ROR-1 L (b)
FGF5 (b)
HRGa2 (b)
HRGa1 (b)
MLCK (b)
MMP2 (5b) (b)
MMP-2 (b)
MMP2 (5a) (b)
PDGF-Rb L (b)
TKT L (b)
FGF2 (b)
fyn L (b)
Caveolin2 (b)
M-CSF (b)
Caveolin1 (b)
MMP14 (12a) (b)
Ufo/axl (b)
Ufo/axl L (b)
PA I (b)
Vimentin (b)
ADAM12 (d)
ADAM12 (b)
NDF-1 (b)
MT3MMP (b)
EPHA2 L (b)
HBEGF (b)
DR5 (b)
SIRPanha1 (b)
lyn L (b)
lyn (b)
ADAM17 (d)
ADAM17 (b)
KIAA0687 (b)
SGK (h) (b)
PAP (b)
MMP-1 (b)
annexin (b)
META-1 (b)
CD44 (b)
TIMP1 (1c) (b)
TIMP1 (1b) (b)
Highly-invasive
Normal
Weakly-invasive

Fig. 3A


1.
2.
3.
MDA-MB157F4xER-
HBL100F4-ER-
MDA-MB435SF4-ER-
MDA-MB415F4-Erx
MDA-MB231F4-ER-
MDA-MB436F4-ER-
Hs578TF4xER-
BT549F4-ER-
Ac-745F4-ER+
MCF10AF4-ER-
HUVEC
MDA-MB453F4+ER-
ZR75-30F4-Erx
MDA-MB361F4+ER+
MCF7(Su)F4+ER+
BT483F4+Erx
T47DF4+ER+
ZR75-1F4+ER+
DBLF4-Erx
BT474F4-ER+
SKBR3F4+ER-
BT20F4-ER-
MDA-MB468F4-ER-
MDA-MB175F4-ER-
DU-44-75F4+Erx
Placenta
BC3640duT2N1M0II+F4-
BC181duT1N1M0II-65F4x
BC3539duT2N1M0II+73F4-
BC3638duT1N1M0II+F4+
BC3637loT2N1M0II+57F4-
BC3632duT2N0M0II+44F4+
BC8335intraduTxNxMxIII-57F+
BC9354duT2N2M0IIIa-49F4-
BC6735duT2N0M1IV-37F4+
BC168duT2N0M0II+74F4x
BC177duT2N1M0II+61F4x
BC8786duT1N2M0II+F4+
BC159duT1N0M0I-29F4x
BC5382duT4N2M0IIIb-56F4+*
BC13232duT2N4M0IIII-61F4-
BC14724duT2N2M0IIII-F4-
BC9796duT2N0M0II+46F4-
BC13316duT2N2M0IIII+71F4-
BC80duT2N0M0II-62F4x
BC8566intraduTxNxMx-68F4-
BC10150duT2N4M0IIII-69F4+
BC8114duT4N2MxIII+35F4+
BC14879duT3N0M0IIIb+46F4-
BC11218duT2N3M2IV+59F4-*
BC10555duT2N0M0II+77*
BC12166duM2N2M0IIIIb+45F4+
BC10681duT1N0M0I-51F4+
BC8481duT2N2M0IIII-57F4+*
BC13932duT4N2M0IIIIb-45F4+
BC16353duT4N4M0IIII-51F4-
BC11697duloT2N4M0IIII+67F4+*
Blood PMN
Blood MNC
BC184duT1N0M0I-80F4x
BC3433duT2N0M0II+72F4-
BC151duTxN1M0II-61F4x
BC11820duT4N4M0IIII-41F4-
BC10670dupapT2N4M0IIII+82F4-
P991NormBrF4-
P1356NormBr
P15856NormBr
P19044NormBr
P14860NormBr
P15153NormBrF4-
BC176duT1N0M0I+76F4x
BC3631loT4N8M0+61F4+
BC183duT2N0M0II+41F4x
Corr: 0.51
TKT L (b)
CD44 (b)
TIMP3 (3a) (b)
EDG2 (b)
Caveolin2 (b)
Caveolin1 (b)
TIMP2 (2b) (b)
Ufo/axl L (b)
MMP14 (12a) (b)
ADAM12 (d)
M-CSF (b)
lyn L (b)
fyn L (b)
SIRPapha1 (b)
Gas6 (b)
FGF1 (b)
Stat5b (b)
Stat5a (b)

TKT L (b)
EDG2 (b)
FGF1 (b)
Stat5b (b)
Stat5a (b)
Gas6 (b)
Ufo/Axl L (b)
MMP14 (12a) (b)
ADAM12 (d)
MMP2 (5b) (b)
Vimentin (b)
TIMP3 (3a) (b)
HDEGF (b)
EPHA2 L (b)
ADAM17 (b)
abl L (b)
M-CSF (b)
Caveolin2 (b)
Caveolin1 (b)
CD44 (b)
SGK (b) (b)
fyn L (b)
lyn L (b)
SIRPaoha1 (b)
S6KII (b)
MMP-1 (b)

Fig. 3B

Analysis of expression RTK AXL and GAS by Northern blot

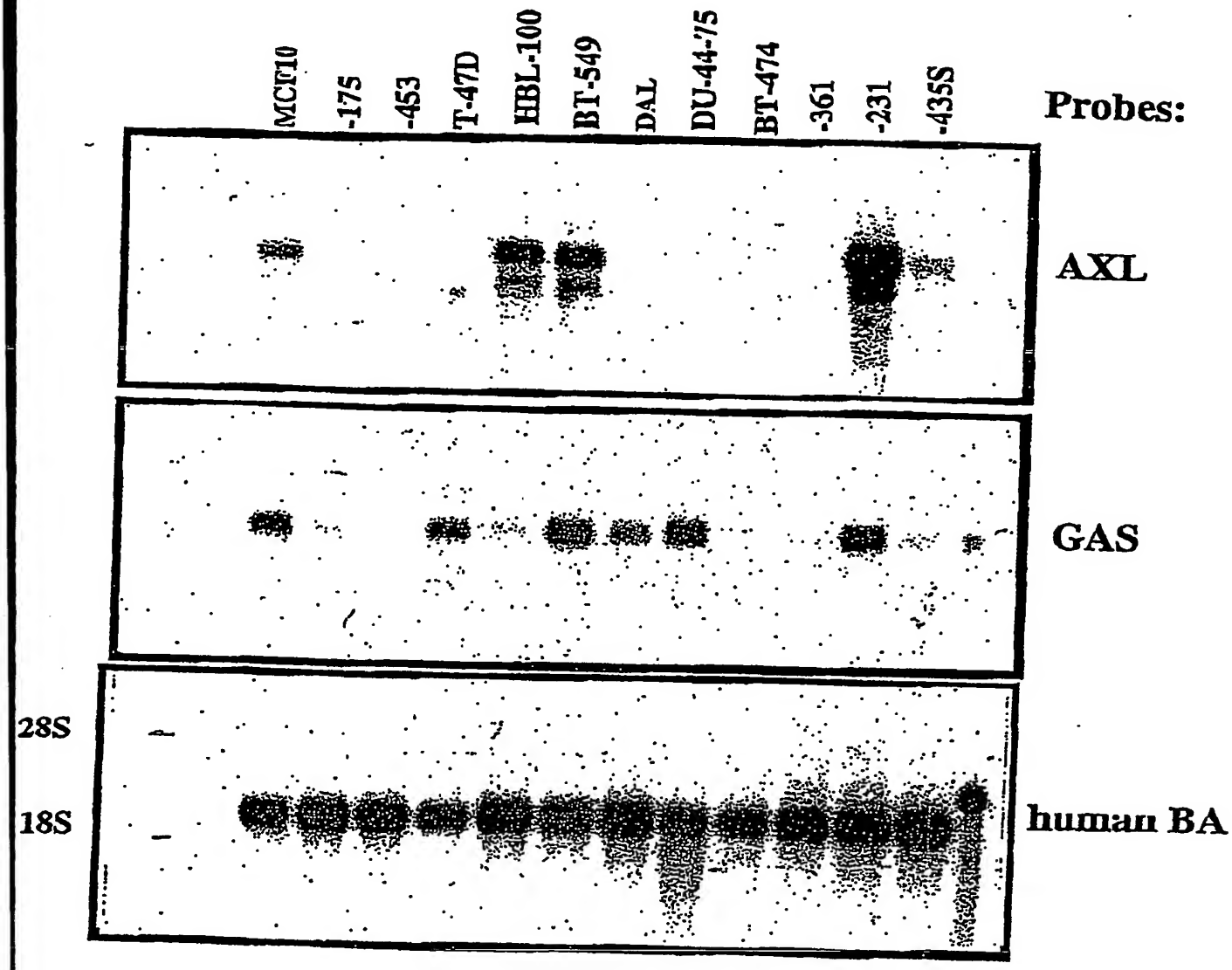


Fig. 4

The 3D outgrowth on Matrigel matrix a different invasive breast cancer cell lines (14 days)

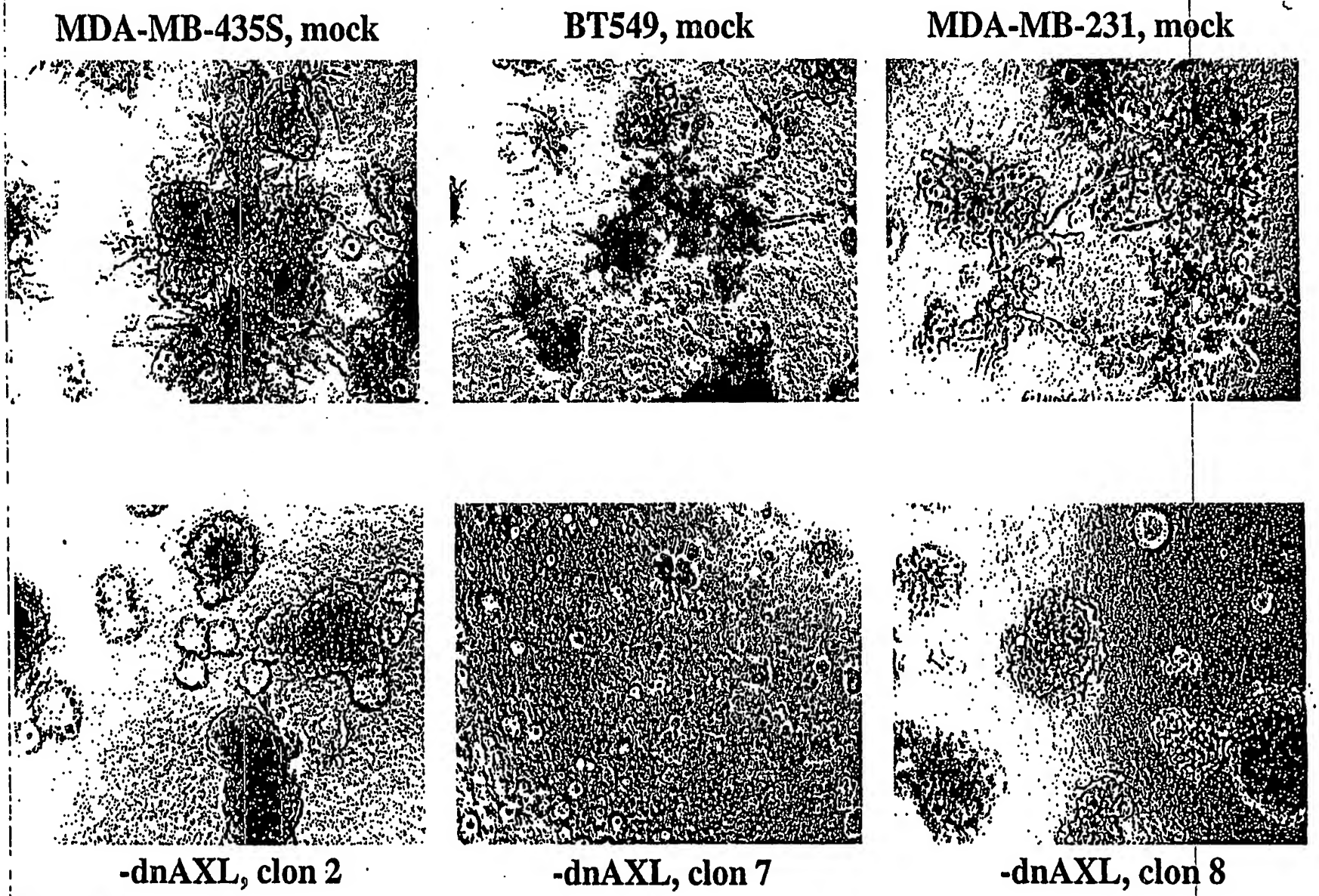


Fig. 5A All -dn-AXL clones growth as non invasive, pseudo acinar-fused cancer cells x100

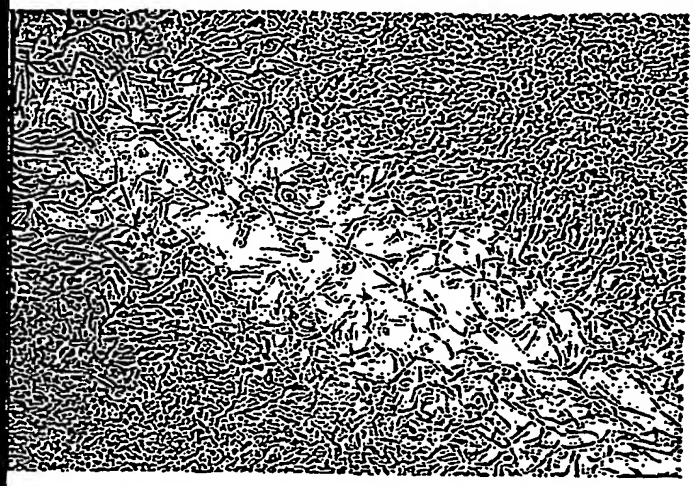
Fig. 5B

Wound assay

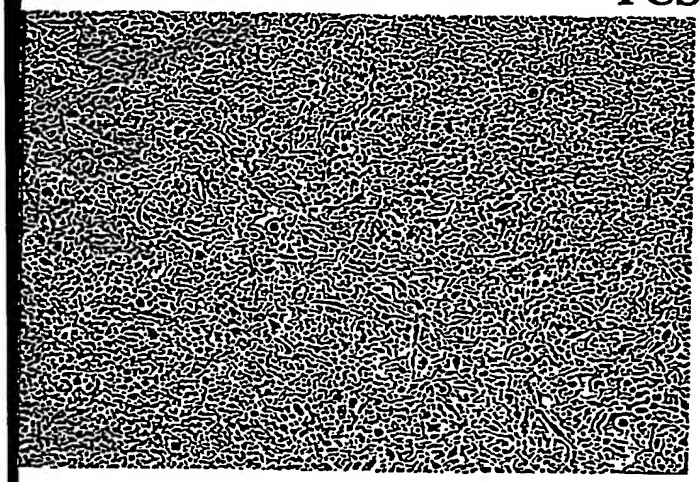
MDA-MB-435S, mock

10%FCS

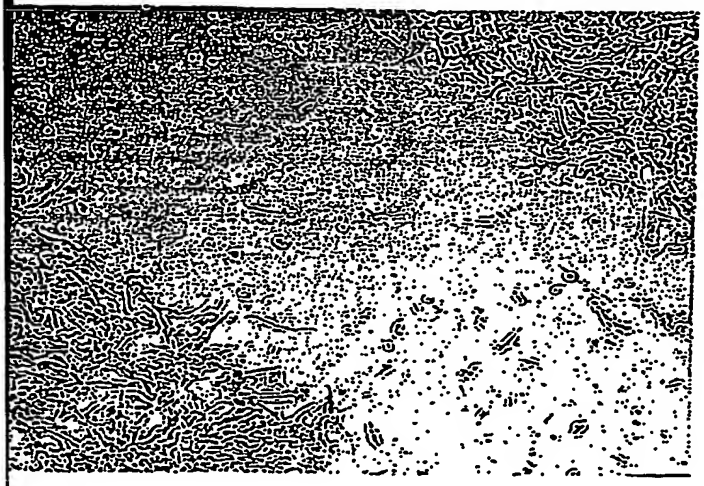
MDA-MB435S-dnAXL, cl. 2



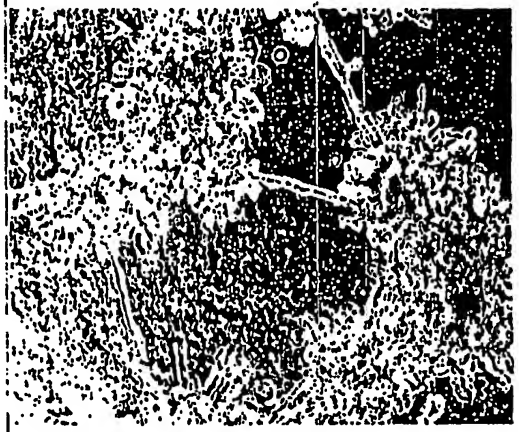
FCS+GAS6



Starvation 72h



MDA-MB-435S, mock treated by Ex-AXL antibody (ab): 3D growth on MM, 14 days

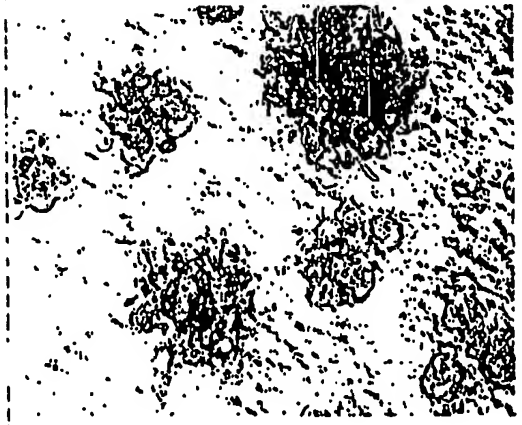


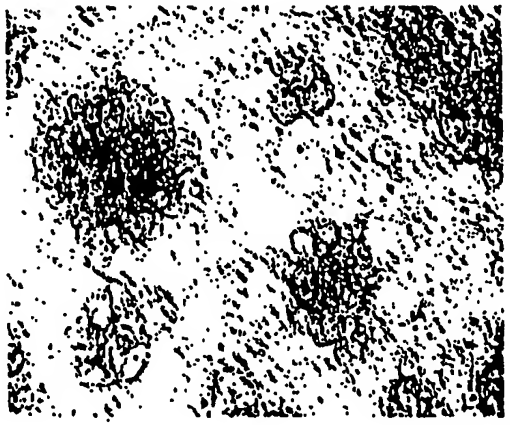
no ab treatment

+anti-GAS ab

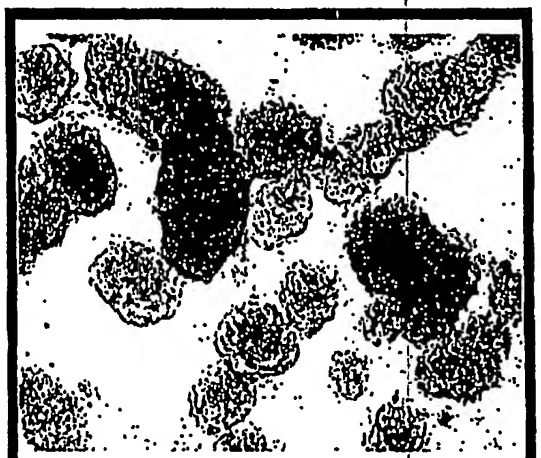
+preimmune serum (R1)

(MDA-MB435S-dnAXL cl2, 14 days on MM)





treatment by -Ex-AXL ab: fused outgrowth



(pseudo acinar or fused)

Fig. 6A

x100 all

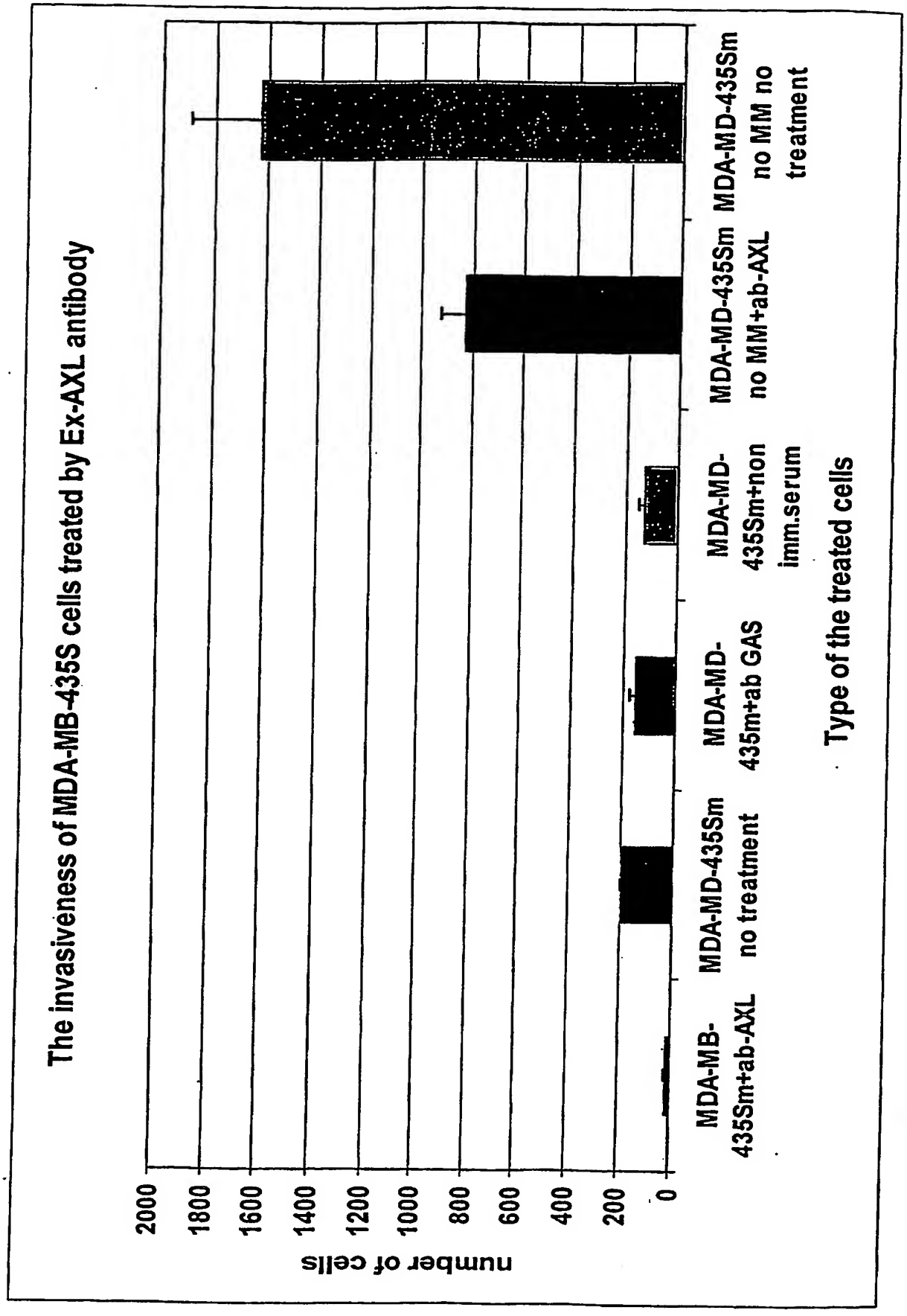

The invasiveness of MDA-MB-435S cells treated by Ex-AXL antibody
number of cells
2000
1800
1600
1400
1200
1000
800
600
400
200
0
MDA-MB-435Sm+ab-AXL
MDA-MD-435Sm no treatment
MDA-MD-435m+ab GAS
MDA-MD-435Sm+non imm.serum
MDA-MD-435Sm no MM+ab-AXL
MDA-MD-435Sm no MM no treatment
Type of the treated cells

Fig. 6B

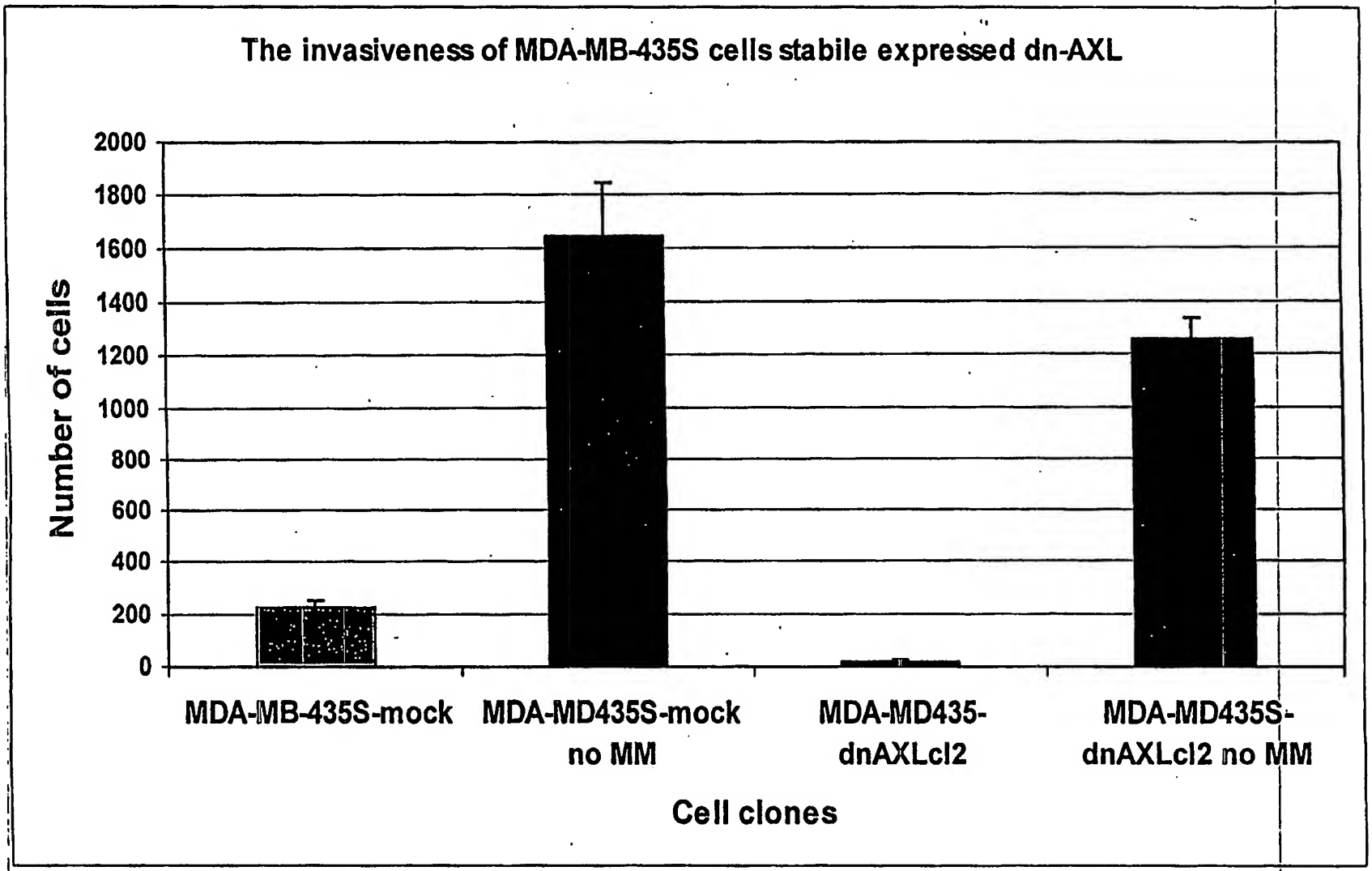

The invasiveness of MDA-MB-435S cells stabile expressed dn-AXL
Number of cells
2000
1800
1600
1400
1200
1000
800
600
400
200
0
MDA-MB-435S-mock
MDA-MD435S-mock no MM
MDA-MD435-dnAXLcl2
MDA-MD435S-dnAXLcl2 no MM
Cell clones

Fig. 6C

The morphology of breast cancer cell line MCF7 with forced over-expression RTK AXL wt

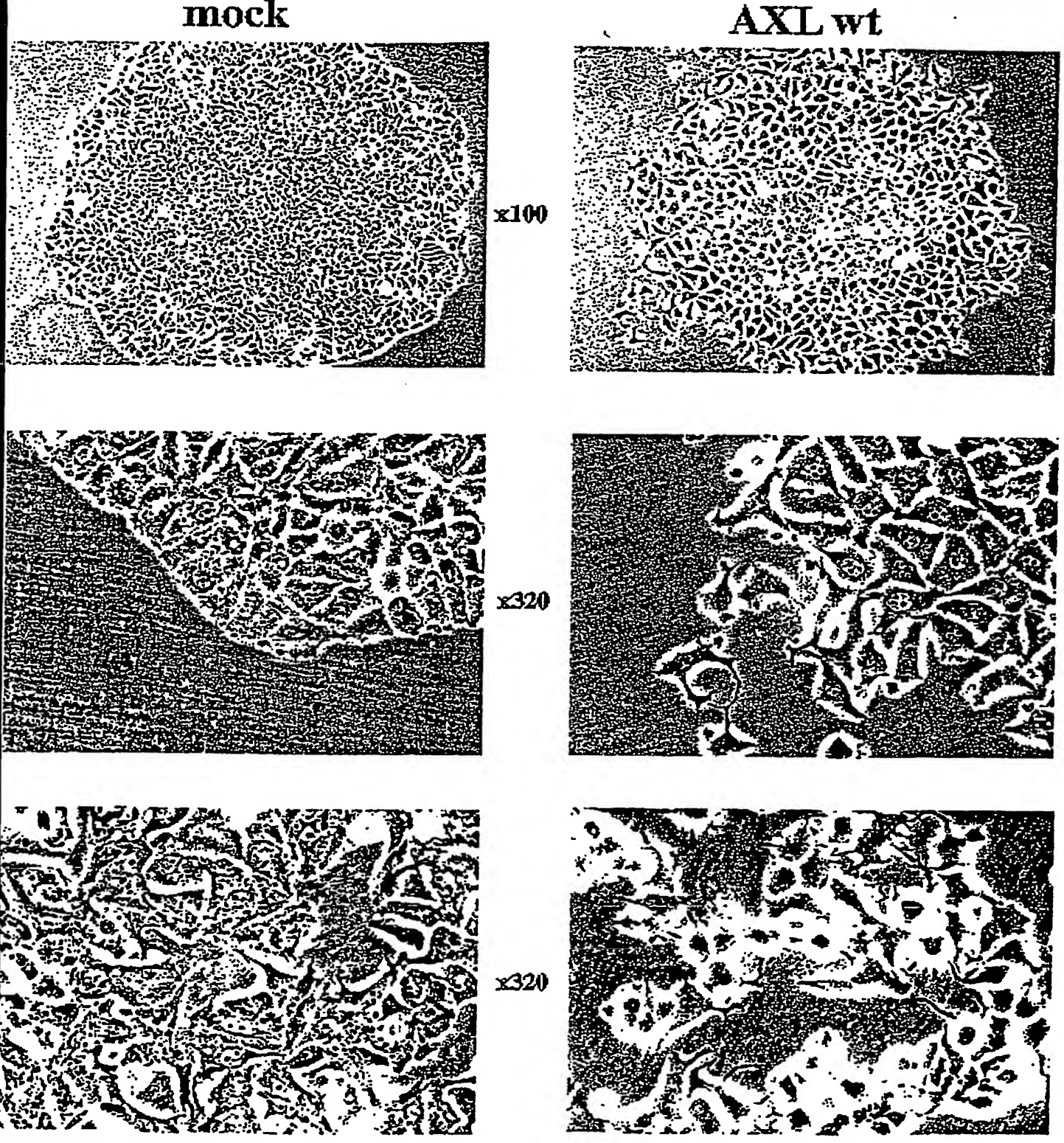


Fig.7A

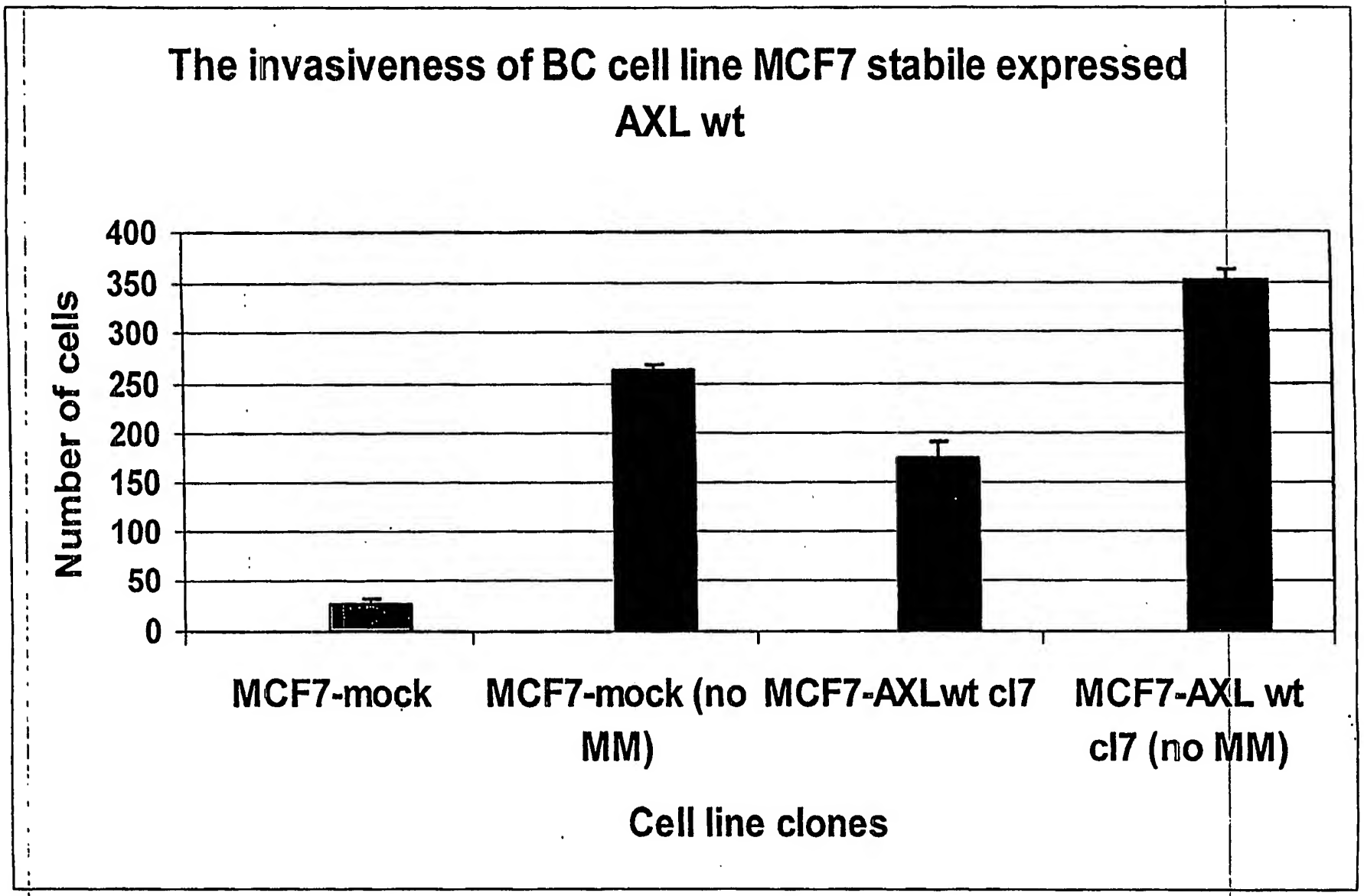

The invasiveness of BC cell line MCF7 stabile expressed AXL wt
Number of cells
400
350
300
250
200
150
100
50
0
MCF7-mock
MCF7-mock (no MM)
MCF7-AXLwt cl7
MCF7-AXL wt cl7 (no MM)
Cell line clones

Fig. 7B

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